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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No. 10/542,558	Applicant(s) CHEN ET AL.	
	Examiner Stephanie K. Mummert, Ph.D.	Art Unit 1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 13 November 2007.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-41 is/are pending in the application.
- 4a) Of the above claim(s) 10, 13 and 17-41 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-9, 11, 12 and 14-16 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date <u>10/19/07</u> . | 6) <input type="checkbox"/> Other: _____ |

DETAILED ACTION

Election/Restrictions

Applicant's election without traverse of Group I, claims 1-9, 11-12 and 14-16 in the reply filed on November 13, 2007 is acknowledged.

It is noted that the previous restriction requirement incorrectly applied US restriction practice to the claims as originally filed under 35 U.S.C. 371. The grouping of the claims remains the same, however the reason for restriction between the groups is different. Claims in cases filed under 35 U.S.C. 371 are restricted according to lack of unity practice. For clarification purposes, the restriction requirement rewritten in view of the lack of unity standard, is restated below. As the grouping of claims is the same in both requirements, the election of the claims for examination is the same.

Restriction is required under 35 U.S.C. 121 and 372.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In accordance with 37 CFR 1.499, applicant is required, in reply to this action, to elect a single invention to which the claims must be restricted.

Group 1, claim(s) 1-9, 11-12, 14-16, drawn to an isolated nucleic acid, expression vector or host cell.

Group 2, claim(s) 10, 13, 30-31, drawn to a method for producing a polypeptide.

Group 3, claim(s) 17-18, drawn to an isolated polypeptide.

Group 4, claim(s) 19, drawn to a purified antibody.

Group 5, claim(s) 20-29, 34-35, drawn to a method a method of detecting BCRM-1 polypeptide.

Group 6, claim(s) 32-33, drawn to a method for targeting a proliferative disorder comprising detecting nucleic acids.

Group 7, claim(s) 36-37, drawn to a method for screening for a therapeutic agent.

Group 8, claim(s) 38-39, drawn to a cell system for screening for therapeutic agents.

Group 9, claim(s) 40-41, drawn to a method for making an antibody.

The inventions listed as Groups 1-9 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The groups are not unified by a special technical feature that distinguishes over the prior art. The claims are directed primarily to SEQ ID NO:2 and products and methods surrounding this polypeptide sequence. However, this sequence does not distinguish over the prior art. Tang et al. (WO02070539; September 2002) teaches a sequence, SEQ ID NO:1018, which has 100% identity to the polypeptide of SEQ ID NO:2. Therefore, there is no unifying or corresponding special technical feature that links the claims together for examination purposes.

A provisional election was made without traverse to prosecute the invention of Group 1, claims 1-9, 11-12, 14-16 in the reply filed on November 13, 2007. Affirmation of this election must be made by applicant in replying to this Office action.

Claims 10, 13, 17-41 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on November 13, 2007.

Claims 1-9, 11-12, 14-16 are pending and will be examined.

Information Disclosure Statement

The information disclosure statement (IDS) submitted on October 19, 2007 was filed in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statement is being considered by the examiner.

Specification

The disclosure is objected to because of the following informalities: On page 1, at the very beginning of the second paragraph under the 'Background' heading, multiple words are missing from the text. Appropriate correction is required.

Claim Interpretation

The term degenerate variant is being given the broadest reasonable interpretation in view of the specification. The term is not defined in any way and instead simply referred to as "an isolated nucleic acid having the nucleotide sequence of SEQ ID NO:1 or its degenerate variant" (p. 2 of PgPub, paragraph 11). Therefore, the term is being given a broad interpretation, including nucleic acids that are less than 100% identical to the nucleic acid of SEQ ID NO:1, but yet encode the same amino acid(s).

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

1. Claims 1-3, 5 and 14-16 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Legal Analysis

In analysis of the claims for compliance with the written description requirement of 35 U.S.C. 112, first paragraph, the written description guidelines note regarding genus/species situations that "Satisfactory disclosure of a ``representative number" depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (See: Federal Register: December 21, 1999 (Volume 64, Number 244), revised guidelines for written description.)

These claims are directed to nucleic acids encoding a polypeptide at least 70, 80, or 90% identical to SEQ ID NO:2. The claims are also directed to nucleic acid probes which are 'capable of binding' under low, middle, and high stringency to nucleic acids with the target sequence of SEQ ID NO:1, or a complement thereof.

Therefore, the claims encompass a genus of nucleic acids that have any degree of complementarity to SEQ ID NO:1. The genus also includes variants of SEQ ID NO:1 or 2 for

which no written description is provided in the specification. This large genus is represented in the specification by only SEQ ID NO: 1 (nucleic acid) and SEQ ID NO:2 (amino acid). Thus, applicant has express possession of only one particular nucleic acid sequence in a genus, where even 70% homologous sequence will comprise hundreds of millions of different possibilities. Here, no common element or attributes of the sequences are disclosed, not even the presence of certain domains.

Not only are there no structural limitations or requirements which provide guidance on the identification of nucleic acids related to SEQ ID NO: 1 or SEQ ID NO:2, but there are no functional limitations in the claim either. Thus, these claims fail on both prongs of the written description analysis since there is no function for the broad structures to define.

It is noted in the recently decided case The Regents of the University of California v. Eli Lilly and Co. 43 USPQ2d 1398 (Fed. Cir. 1997) decision by the CAFC that

“A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. See *Fiers*, 984 F.2d at 1169- 71, 25 USPQ2d at 1605- 06 (discussing *Amgen*). It is only a definition of a useful result rather than a definition of what achieves that result. Many such genes may achieve that result. The description requirement of the patent statute requires a description of an invention, not an indication of a result that one might achieve if one made that invention. See *In re Wilder*, 736 F.2d 1516, 1521, 222 USPQ 369, 372- 73 (Fed. Cir. 1984) (affirming rejection because the specification does “little more than outlin[e] goals appellants hope the claimed invention achieves and the problems the invention will hopefully ameliorate.”). Accordingly, naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material. “

In the current situation, the definition of the protein by percent homology lacks any specific required structure. This is precisely the situation of naming a type of material which is generally known to likely exist, but, except for the specific sequence comprising SEQ ID NO: 1 and 2, is in the absence of knowledge of the material composition and fails to provide descriptive support

for the generic claim.

Absence of a representative number of species

In the current case, the first question is what constitutes a generic claim. The genus of nucleic acids includes any nucleic acid with any degree of homology across the entire nucleic acid sequence of 1273 residues comprising SEQ ID NO:1, nucleic acids with as few as 2, 12, or 24 for example, contiguous nucleotides homologous to SEQ ID NO:1, or nucleic acids which comprise ‘a complement thereof’ of nucleic acids which represent allelic variants of SEQ ID NO:1. Thus, the claim reads on a multitude of nucleic acids, including sequences which themselves may not yet be described in the scientific literature. In order to provide a representative number of species, in a genus which contains literally hundreds of billions of different members, the court in Lilly required “A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus. (Lilly at page 1406).” Lilly continues to note that in other cases, two chemical compounds in a subgenus were insufficient to describe that genus. In the current case, only two species are disclosed, SEQ ID NO:1 and 2. These species represent a specific nucleic acid sequence and the amino acid it encoded and are not representative of the entire genus.

Absence of any structure-function relationship

The second issue is whether there is any structure function relationship which correlates a function with a particular structure. This question fundamentally addresses the issue of whether there is any structure which the specification demonstrates is necessarily correlated with the probe functions of the nucleic acid of SEQ ID NO:1 or the known function of the polypeptide of SEQ ID NO:2 as a breast cancer resistance marker (BCRM-1). In this case, the answer is no, there is no structure given, other than SEQ ID NOs:1 and 2.

Since there is no common structure among the nucleic acids that are specifically associated with the unknown function of the nucleic acid, except for a role as a primer or probe, there is no structure-function relationship between the genus of nucleic acids claimed.

The claim scope broadly encompasses any nucleotide sequence with homology to SEQ ID NO:1 or SEQ ID NO:2

The claims are open to any nucleic acid sequence, whether currently known or not. For this vast genus, only one species is provided. Thus, the conclusion is inescapable that the specification fails to provide a representative number of species in the genus of nucleic acid sequences that share any degree of homology or complementarity across the entire nucleic acid sequence of 1273 residues comprising SEQ ID NO:1, or nucleic acids which comprise 'a complement thereof' of nucleic acids which represent allelic variants of SEQ ID NO:1 and nucleic acids which encode amino acids with homology to SEQ ID NO:2.

Conclusion

In the application at the time of filing, there is no record or description which would demonstrate conception of any nucleic acid sequences other than those expressly disclosed which

Db 386 CTGCCTTTCATGGCGCCACGGTATTTTGTCAATGACGCCACTGAAAGGGATCAAGTCC 445

Qy 304 GTGATTTTACCTCAGGTTTTCTCTGTGCCTACATGGCAGCGTTCAACAGCATCAATGGA 363
|||||

Db 446 GTGATTTTACCTCAGGTTTTCTCTGTGCCTACATGGCAGCGTTCAACAGCATCAATGGA 505

Qy 364 AACAGAAGTTACACTTGTAAGCCACTAGAAAGATCATTACTAATGGCGGGAGCCGTTGCT 423
|||||

Db 506 AACAGAAGTTACACTTGTAAGCCACTAGAAAGATCATTACTAATGGCGGGAGCCGTTGCT 565

Qy 424 TCTTCAACTTTCTTAGGAGTAATCCCTCAGTTTGTCCAGATGAAGTATGGCCTGACTGGC 483
|||||

Db 566 TCTTCAACTTTCTTAGGAGTAATCCCTCAGTTTGTCCAGATGAAGTATGGCCTGACTGGC 625

Qy 484 CCTTGGATTAAAAGACTCTTACCTGTGATCTTCCTCGTGCAAGCCAGTGGAATGAATGTC 543
|||||

Db 626 CCTTGGATTAAAAGACTCTTACCTGTGATCTTCCTCGTGCAAGCCAGTGGAATGAATGTC 685

Qy 544 TACATGTCCCGAAGTCTTGAATCCATTAAGGGGATTGCGGTCATGGACAAGGAAGGCAAT 603
|||||

Db 686 TACATGTCCCGAAGTCTTGAATCCATTAAGGGGATTGCGGTCATGGACAAGGAAGGCAAT 745

Qy 604 GTCCTGGGTCATTCCAGAATTGCTGGGACAAAGGCTGTTAGAGAAACGCTAGCATCCAGA 663
|||||

Db 746 GTCCTGGGTCATTCCAGAATTGCTGGGACAAAGGCTGTTAGAGAAACGCTAGCATCCAGA 805

Qy 664 ATAGTGCTGTTTGGGACCTCAGCTCTGATTCTGAAGTCTTCACCTACTTTTTTAAAAGG 723
|||||

Db 806 ATAGTGCTGTTTGGGACCTCAGCTCTGATTCTGAAGTCTTCACCTACTTTTTTAAAAGG 865

Qy 724 ACCCAGTATTTTACAGGAAAACCCAGGGTCATTGTGGATTTTGAAACTGTCTTGTACTGTC 783
|||||

Db 866 ACCCAGTATTTTACAGGAAAACCCAGGGTCATTGTGGATTTTGAAACTGTCTTGTACTGTC 925

Qy 784 CTGGCAATGGGACTGATGGTGCCATTTTCTTTTAGTATATTTCCACAGATTGGACAGATA 843
|||||

Db 926 CTGGCAATGGGACTGATGGTGCCATTTTCTTTTAGTATATTTCCACAGATTGGACAGATA 985

Qy 844 CAGTACTGTAGTCTTGAAGAGAAAATTCAGTCTCCAACAGAAGAAACAGAAATCTTTTAT 903
|||||

Db 986 CAGTACTGTAGTCTTGAAGAGAAAATTCAGTCTCCAACAGAAGAAACAGAAATCTTTTAT 1045

Qy 904 CACAGAGGGGTGTAGG-CGTGAGTTTTAGGTGAATTTATGTGGTT-CCTGCTTGAAAACC 961
|||||

Db 1046 CACAGAGGGGTGTAGGCCGTGAGTTTTAGGTGAATTTATGTGGTTCCCTGCTTGAAAACC 1105

Qy 962 TTCCCC--TCTCCAGGTTTCGGTTTAGAGAACTTTG-CCACAGGTCTTCTGGGGACCCAG 1018
|||||

Db 1106 TTCCCCCTCTCCAGGTTTCGGTTTAGAGAACTTTGCCACAGGTCTTCTGGGGACCCAG 1165

Qy 1019 AGGTGTCTGTGCTGACAAGGCGACTTCAGATTCCATACTGAGATCGTTCCAGGCTGGCG 1078
|||||

Db 1166 AGGTGTCTGTGCTGACAAGGCGACTTCAGATTCCATACTGAGATCGTTCCAGGCTGGCG 1225

Qy 1079 TCTCTGGGGTTTTTAAGGCTGGCTGGAGAAGACAGTGGG-AGGGTGCCCCGTCTGACACC 1137
|||||

Db 1226 TCTCTGGGGTTTTTAAGGCTGGCTGGAGAAGACAGTGGGAAGGGTGCCCCGTCTGACACC 1285

Qy 1138 CCTGGGGTTGCTGAGGGAACGGTTGGAGTGGGGATCGGCCTGCGAAAGGATACTGTGAAA 1197

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      |||
Db      1286 CCTGGGGTTGCTGAGGGAACGTTGGAGTGGGGATCGGCCTGCGAAAGGATACTGTGAAA 1345
      |||
Qy      1198 TCACTAATTAAC TAATAAACCTGTCTCAAGTTGAGGATTTAAGGGAGGTCAAA 1250
      |||
Db      1346 TCACTAATTAAC TAATAAACCTGTCTCAAGTTGAGGATTTGAAGAAAAAAAAA 1398
      |||

AMINO ACID - SEQ ID NO:899 of Tang

Qy      1  MAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSYTCKPLERSLLMAGAVASST 60
      |||
Db      132 MAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSYTCKPLERSLLMAGAVASST 191
      |||
Qy      61  FLGVIPQFVQMKYGLTGPWIKRLLPVI FLVQASGMNVYMSRSLESIKGIAMVDKEGNVLG 120
      |||
Db      192 FLGVIPQFVQMKYGLTGPWIKRLLPVI FLVQASGMNVYMSRSLESIKGIAMVDKEGNVLG 251
      |||
Qy      121 HSRIAGTKAVRETLASRIVLFGTSALIP EVFTYFFKRTQYFRKNPGSLWILKLSCTVLAM 180
      |||
Db      252 HSRIAGTKAVRETLASRIVLFGTSALIP EVFTYFFKRTQYFRKNPGSLWILKLSCTVLAM 311
      |||
Qy      181 GLMVPFSSFSIFPQIGQIQYCSLEEKIQSPTEETEIFYHRGV 221
      |||
Db      312 GLMVPFSSFSIFPQIGQIQYCSLEEKIQSPTEETEIFYHRGV 352
      |||

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With regard to claim 6, Tang teaches an isolated nucleic acid comprising the nucleotide sequence of SEQ ID NO: 1 or a degenerate variant thereof (see alignment above of nucleic acid of SEQ ID NO:160 of Tang, encoding an amino acid which is 100% identical to SEQ ID NO:2, which is a degenerate variant of SEQ ID NO:1 as it encodes the same amino acid sequence).

With regard to claim 7, Tang teaches an isolated nucleic acid comprising a sequence that encodes a polypeptide with the amino acid sequence of SEQ ID NO:2 (see alignment above of nucleic acid of SEQ ID NO:160 of Tang, encoding an amino acid 100% identical to SEQ ID NO:2, which is a degenerate variant of SEQ ID NO:1).

With regard to claim 8, Tang teaches an expression vector comprising the nucleic acid of claim 7 operably linked to an expression control sequence (p. 2, lines 5-9; p. 3, lines 8-10; p. 8, lines 12-19; p. 8, lines 12-19, where the nucleic acids are operably linked to an expression control sequence; p. 10, lines 20-26, where the term operably linked is defined).

With regard to claim 9, Tang teaches a cultured cell comprising the expression vector of claim 8 (p. 3, lines 8-10, where the expression vector is transformed into cells; p. 4, lines 21-27, where the cells are cultured and the polypeptide is isolated).

With regard to claim 11, Tang teaches a cultured cell transfected with the vector of claim 7, or a progeny of the cell, wherein the cell expresses a polypeptide encoded by the expression vector (where the expression vector is transformed into cells; p. 4, lines 21-27, where the cells are cultured and the polypeptide is isolated).

With regard to claim 12, Tang teaches a cultured cell comprising the nucleic acid of claim 7 operably linked to an expression control sequence (p. 8, lines 12-19, where the nucleic acids are operably linked to an expression control sequence; p. 10, lines 20-26, where the term operably linked is defined).

With regard to claim 14, Tang teaches an isolated nucleic acid comprising a sequence that hybridizes under low stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO: 1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 1, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

With regard to claim 15, Tang teaches an isolated nucleic acid comprising a sequence that hybridizes under medium stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO:1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 1, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

With regard to claim 16, Tang teaches an isolated nucleic acid comprising a sequence that hybridizes under high stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO: 1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 1, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

3. Claims 1-4, 6-9, 11-12 and 14-16 are rejected under 35 U.S.C. 102(e) as being anticipated by Tang et al. (WO02070539; September 2002). Tang teaches the isolation of nucleic acids and polypeptides (Abstract).

With regard to claim 1, 2, 3, 4, Tang teaches an isolated nucleic acid encoding a polypeptide comprising an amino acid sequence which is at least 70%, 80%, 90% or 95% identical to the amino acid sequence of SEQ ID NO:2 (see alignment below where the amino acid of SEQ ID NO:1018 has 100% identity with SEQ ID NO:2 and see Table 8, p. 992 where the amino acid is encoded by nucleic acid comprising SEQ ID NO:70, see alignment attached at claim 6 below).

```
Qy      1  MAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSYTCKPLERSLLMAGAVASST  60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSYTCKPLERSLLMAGAVASST  60

Qy     61  FLGVIPQFVQMKYGLTGPWIKRLLPVI FLVQASGMNVYMSRSLESIKGIAVMDKEGNVLG  120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  FLGVIPQFVQMKYGLTGPWIKRLLPVI FLVQASGMNVYMSRSLESIKGIAVMDKEGNVLG  120

Qy    121  HSRIAGTKAVRETLASRIVLFGTSALIP EVFTYFFKRTQYFRKNPGSLWILKL SCTVLAM  180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  HSRIAGTKAVRETLASRIVLFGTSALIP EVFTYFFKRTQYFRKNPGSLWILKL SCTVLAM  180

Qy    181  GLMVPF SFSIFPQIGQIQYCSLEEKIQSPTEETEIFYHRGV  221
      ||||||||||||||||||||||||||||||||||||||||
Db    181  GLMVPF SFSIFPQIGQIQYCSLEEKIQSPTEETEIFYHRGV  221
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With regard to claim 6, Tang teaches an isolated nucleic acid comprising the nucleotide sequence of SEQ ID NO: 1 or a degenerate variant thereof (see alignment, where SEQ ID NO:1 of Tang comprises a degenerate variant of SEQ ID NO:1 as it encodes the same amino acid as SEQ ID NO:2).

Qy	184	GCAACAGTGCATCCCGACAGCAGCAACCTGATCCCCAAGCTTTTTCGACCTGCAGCGTTC	243
Db	26	GCAACAGTGCATCCCGACAGCAGCAACCTGATCCCCAAGCTTTTTCGACCTGCAGCGTTC	85
Qy	244	CTGCCTTTTCATGGCGCCACGGTATTTTGTCAATGACGCCACTGAAAGGGATCAAGTCC	303
Db	86	CTGCCTTTTCATGGCGCCACGGTATTTTGTCAATGACGCCACTGAAAGGGATCAAGTCC	145
Qy	304	GTGATTTTACCTCAGGTTTTCCTCTGTGCCTACATGGCAGCGTTCAACAGCATCAATGGA	363
Db	146	GTGATTTTACCTCAGGTTTTCCTCTGTGCCTACATGGCAGCGTTCAACAGCATCAATGGA	205
Qy	364	AACAGAAGTTACACTTGTAAAGCCACTAGAAAGATCATTACTAATGGCGGGAGCCGTTGCT	423
Db	206	AACAGAAGTTACACTTGTAAAGCCACTAGAAAGATCATTACTAATGGCGGGAGCCGTTGCT	265
Qy	424	TCTTCAACTTTCTTAGGAGTAATCCCTCAGTTTGTCCAGATGAAGTATGGCCTGACTGGC	483
Db	266	TCTTCAACTTTCTTAGGAGTAATCCCTCAGTTTGTCCAGATGAAGTATGGCCTGACTGGC	325
Qy	484	CCTTGGAATTTAAAGACTCTTACCTGTGATCTTCCTCGTGCAAGCCAGTGAATGAATGTC	543
Db	326	CCTTGGAATTTAAAGACTCTTACCTGTGATCTTCCTCGTGCAAGCCAGTGAATGAATGTC	385
Qy	544	TACATGTCCCGAAGTCTTGAATCCATTAAGGGGATTGCGGTATGGACAAGGAAGGCAAT	603
Db	386	TACATGTCCCGAAGTCTTGAATCCATTAAGGGGATTGCGGTATGGACAAGGAAGGCAAT	445
Qy	604	GTCCTGGGTCAATTCAGAATTGCTGGGACAAAGGCTGTTAGAGAAACGCTAGCATCCAGA	663
Db	446	GTCCTGGGTCAATTCAGAATTGCTGGGACAAAGGCTGTTAGAGAAACGCTAGCATCCAGA	505
Qy	664	ATAGTGCTGTTTGGGACCTCAGCTCTGATTCCCTGAAGTCTTCACCTACTTTTTTAAAGG	723
Db	506	ATAGTGCTGTTTGGGACCTCAGCTCTGATTCCCTGAAGTCTTCACCTACTTTTTTAAAGG	565
Qy	724	ACCCAGTATTTTCAGGAAAAACCCAGGGTCATTGTGGATTTTGAAACTGTCTTGTACTGTC	783
Db	566	ACCCAGTATTTTCAGGAAAAACCCAGGGTCATTGTGGATTTTGAAACTGTCTTGTACTGTC	625
Qy	784	CTGGCAATGGGACTGATGGTGCCATTTCTTTTAGTATATTTCCACAGATTGGACAGATA	843
Db	626	CTGGCAATGGGACTGATGGTGCCATTTCTTTTAGTATATTTCCACAGATTGGACAGATA	685
Qy	844	CAGTACTGTAGTCTTGAAGAGAAAATTCAGTCTCCAACAGAAGAAACAGAAATCTTTTAT	903
Db	686	CAGTACTGTAGTCTTGAAGAGAAAATTCAGTCTCCAACAGAAGAAACAGAAATCTTTTAT	745

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Qy      904 CACAGAGGGGTGTAGGCGTGAGTTTTAGGTGAATTTATGTGGTTCCTGCTTGAAAACCTT 963
          |||
Db      746 CACAGAGGGGTGTAGGCGTGAGTTTTAGGTGAATTTATGTGGTTCCTGCTTGAAAACCTT 805

Qy      964 CCCCTCTCCAGGTCGGTTTAGAGAACTTTGCCACAGGTCTTCTGGGGACCCAGAGGTG 1023
          |||
Db      806 CCCCTCTCCAGGTCGGTTTAGAGAACTTTGCCACAGGTCT----- 846

Qy      1024 TCTGTGCTGACAAGGCGACTTCAGATTCCATACTGAGATCGTTCCTCCAGGCTGGCGTCTCT 1083
          |||
Db      847 -----TCT 849

Qy      1084 GGGGTTTTTAAGGCTGGCTGGAGAAGACAGTGGGAGGGTGCCCCGTCTGACACCCCTGGG 1143
          |||
Db      850 GGGGTTTTTAAGGCTGGCTGGAGAAGACAGTGGGAGGGTGCCCCGTCTGACACCCCTGGG 909

Qy      1144 GTTGCTGAGGGAACGGTTGGAGTGGGGATCGGCCTGCGAAAGGATACTGTGAAATCACTA 1203
          |||
Db      910 GTTGCTGAGGGAACGGTTGGAGTGGGGATCGGCCTGCGAAAGGATACTGTGAAATCACTA 969

Qy      1204 ATTAATAATAAACCTGTCTCAAGTTGAGGATTTAAGGGAGG 1245
          |||
Db      970 ATTAATAATAAACCTGTCTCAAGTTGAGGATTTGAAGAAAG 1011
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With regard to claim 7, Tang teaches an isolated nucleic acid comprising a sequence that encodes a polypeptide with the amino acid sequence of SEQ ID NO:2 (see alignment above where the amino acid of SEQ ID NO:1018 has 100% identity with SEQ ID NO:2 and see Table 8, p. 992, where this amino acid is encoded by SEQ ID NO: 70).

With regard to claim 8, Tang teaches an expression vector comprising the nucleic acid of claim 7 operably linked to an expression control sequence (p. 2, lines 4-7; p. 3, lines 3-5; p. 7, lines 22-28, where the nucleic acids are operably linked to an expression control sequence; p. 9, lines 18-25, where the term operably linked is defined).

With regard to claim 9, Tang teaches a cultured cell comprising the expression vector of claim 8 (p. 3, lines 3-5, where the expression vector is transformed into cells; p. 4, lines 13-19, where the cells are cultured and the polypeptide is isolated).

With regard to claim 11, Tang teaches a cultured cell transfected with the vector of claim 7, or a progeny of the cell, wherein the cell expresses a polypeptide encoded by the expression vector (p. 3, lines 3-5, where the expression vector is transformed into cells; p. 4, lines 13-19, where the cells are cultured and the polypeptide is isolated).

With regard to claim 12, Tang teaches a cultured cell comprising the nucleic acid of claim 7 operably linked to an expression control sequence (p. 7, lines 22-28, where the nucleic acids are operably linked to an expression control sequence; p. 9, lines 18-25, where the term operably linked is defined).

With regard to claim 14, Tang teaches an isolated nucleic acid comprising a sequence that hybridizes under low stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO: 1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 6, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

With regard to claim 15, Tang teaches an isolated nucleic acid comprising a sequence that hybridizes under medium stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO:1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 6, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

With regard to claim 16, Tang teaches an isolated nucleic acid comprising a sequence that hybridizes under high stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO: 1 or the complement of SEQ ID NO: 1 (see alignment associated with

claim 6, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

4. Claims 1-4, 6-9, 11-12 and 14-16 are rejected under 35 U.S.C. 102(a) as being anticipated by Strausberg, et al. (PNAS, 2002, vol. 99, no. 26, p. 16899-16903, e-pub December 2002) as evidenced by Mammalian Gene Collection website (mgc.nci.nih.gov). Strausberg teaches the isolation and analysis of mouse cDNAs (Abstract).

With regard to claim 1, 2, 3 or 4, Strausberg teaches an isolated nucleic acid encoding a polypeptide comprising an amino acid sequence which is at least 70%, 80%, 90% or 95% identical to the amino acid sequence of SEQ ID NO:2 (see alignment, where the amino acid taught by Strausberg is 100% identical to SEQ ID NO:2 and see alignment below where the isolated nucleic acid encoding the polypeptide is taught).

```
Qy      1  MAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSYTCKPLERSLLMAGAVASST  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     117  MAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSYTCKPLERSLLMAGAVASST  176

Qy      61  FLGVIPQFVQMKYGLTGPIKRLLPVIFLVQASGMNVYMSRSLESIKGIAMVDKEGNVLG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     177  FLGVIPQFVQMKYGLTGPIKRLLPVIFLVQASGMNVYMSRSLESIKGIAMVDKEGNVLG  236

Qy     121  HSRIAGTKAVRETLASRIVLFGTSALIEVFYFFKRTQYFRKNPGSLWILKLSCTVLAM  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     237  HSRIAGTKAVRETLASRIVLFGTSALIEVFYFFKRTQYFRKNPGSLWILKLSCTVLAM  296

Qy     181  GLMVPFSFSIFPQIGQIQYCSLEEKIQSPTEETEIFYHRGV  221
          ||||||||||||||||||||||||||||||||||||||||
Db     297  GLMVPFSFSIFPQIGQIQYCSLEEKIQSPTEETEIFYHRGV  337
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With regard to claim 6, Strausberg teaches an isolated nucleic acid comprising the nucleotide sequence of SEQ ID NO: 1 or a degenerate variant thereof (see alignment below

where the nucleic acid comprises a degenerate variant of SEQ ID NO:1 as it encodes the polypeptide of claim 1, 100% identical to SEQ ID NO:2).

Qy	184	GCAACAGTGCATCCCGACAGCAGCAACCTGATCCCCAAGCTTTTTCGACCTGCAGCGTTC	243
Db	296	GCAACAGTGCATCCCGACAGCAGCAACCTGATCCCCAAGCTTTTTCGACCTGCAGCGTTC	355
Qy	244	CTGCCTTTCATGGCGCCACGGTATTTTGTCAATGACGCCACTGAAAGGGATCAAGTCC	303
Db	356	CTGCCTTTCATGGCGCCACGGTATTTTGTCAATGACGCCACTGAAAGGGATCAAGTCC	415
Qy	304	GTGATTTTACCTCAGGTTTTCCTCTGTGCCTACATGGCAGCGTTCAACAGCATCAATGGA	363
Db	416	GTGATTTTACCTCAGGTTTTCCTCTGTGCCTACATGGCAGCGTTCAACAGCATCAATGGA	475
Qy	364	AACAGAAGTTACACTTGTAAGCCACTAGAAAGATCATTACTAATGGCGGGAGCCGTTGCT	423
Db	476	AACAGAAGTTACACTTGTAAGCCACTAGAAAGATCATTACTAATGGCGGGAGCCGTTGCT	535
Qy	424	TCTTCAACTTTCTTAGGAGTAATCCCTCAGTTTGTCCAGATGAAGTATGGCCTGACTGGC	483
Db	536	TCTTCAACTTTCTTAGGAGTAATCCCTCAGTTTGTCCAGATGAAGTATGGCCTGACTGGC	595
Qy	484	CCTTGGATTAAAAGACTCTTACCTGTGATCTTCTCGTGCAAGCCAGTGAATGAATGTC	543
Db	596	CCTTGGATTAAAAGACTCTTACCTGTGATCTTCTCGTGCAAGCCAGTGAATGAATGTC	655
Qy	544	TACATGTCCCGAAGTCTTGAATCCATTAAGGGGATTGCGGTCATGGACAAGGAAGGCAAT	603
Db	656	TACATGTCCCGAAGTCTTGAATCCATTAAGGGGATTGCGGTCATGGACAAGGAAGGCAAT	715
Qy	604	GTCTGGGTCATTCCAGAATTGCTGGGACAAAGGCTGTTAGAGAAACGCTAGCATCCAGA	663
Db	716	GTCTGGGTCATTCCAGAATTGCTGGGACAAAGGCTGTTAGAGAAACGCTAGCATCCAGA	775
Qy	664	ATAGTGCTGTTTGGGACCTCAGCTCTGATTCTGAAGTCTTACCTACTTTTTTAAAAGG	723
Db	776	ATAGTGCTGTTTGGGACCTCAGCTCTGATTCTGAAGTCTTACCTACTTTTTTAAAAGG	835
Qy	724	ACCCAGTATTTTCAGGAAAAACCCAGGGTCATTGTGGATTTTGAACTGTCTTGTACTGTC	783
Db	836	ACCCAGTATTTTCAGGAAAAACCCAGGGTCATTGTGGATTTTGAACTGTCTTGTACTGTC	895
Qy	784	CTGGCAATGGGACTGATGGTGCCATTTTCTTTTAGTATATTTCCACAGATTGGACAGATA	843
Db	896	CTGGCAATGGGACTGATGGTGCCATTTTCTTTTAGTATATTTCCACAGATTGGACAGATA	955
Qy	844	CAGTACTGTAGTCTTGAAGAGAAAATTCAGTCTCCAACAGAAGAAACAGAAATCTTTTAT	903
Db	956	CAGTACTGTAGTCTTGAAGAGAAAATTCAGTCTCCAACAGAAGAAACAGAAATCTTTTAT	1015
Qy	904	CACAGAGGGGTGTAGGCGTGAGTTTTAGGTGAATTTATGTGGTTCCTGCTTGAAAACCTT	963
Db	1016	CACAGAGGGGTGTAGGCGTGAGTTTTAGGTGAATTTATGTGGTTCCTGCTTGAAAACCTT	1075
Qy	964	CCCCTCTCCAGGTTTCGGTTTAGAGAACTTGCCACAGGTCTTCTGGGGACCCAGAGGTG	1023

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Db      1076 CCCCTCTCCAGGTTTCGGTTTAGAGAACTTTGCCACAGGTCTTCTGGGGACCCCAGAGGTG 1135
Qy      1024 TCTGTGCTGACAAGGCGACTTCAGATTCCATACTGAGATCGTTCCCAGGCTGGCGTCTCT 1083
          |||
Db      1136 TCTGTGCTGACAAGGCGACTTCAGATTCCATACTGAGATCGTTCCCAGGCTGGCGTCTCT 1195
Qy      1084 GGGGTTTTTAAGGCTGGCTGGAGAAGACAGTGGGAGGGTGCCCCGTCTGACACCCCTGGG 1143
          |||
Db      1196 GGGGTTTTTAAGGCTGGCTGGAGAAGACAGTGGGAGGGTGCCCCGTCTGACACCCCTGGG 1255
Qy      1144 GTTGCTGAGGGAACGGTTGGAGTGGGGATCGGCCGCGAAAGGATACTGTGAAATCACTA 1203
          |||
Db      1256 GTTGCTGAGGGAACGGTTGGAGTGGGGATCGGCCGCGAAAGGATACTGTGAAATCACTA 1315
Qy      1204 ATTAATAATAAACCTGTCTCAAGTTGA 1231
          |||
Db      1316 ATTAATAATAAACCTGTCTCAAGTTGA 1343
```

With regard to claim 7, Strausberg teaches an isolated nucleic acid comprising a sequence that encodes a polypeptide with the amino acid sequence of SEQ ID NO:2 (see alignment above where the nucleic acid comprises a degenerate variant of SEQ ID NO:1 as it encodes the polypeptide of claim 1, 100% identical to SEQ ID NO:2).

With regard to claim 8, Strausberg teaches an expression vector comprising the nucleic acid of claim 7 operably linked to an expression control sequence (p. 16899, col. 1, “cDNA library construction” heading, where cDNA libraries were prepared from tissues and cell lines comprising vectors; as evidenced by mgc.nci.nih.gov, where multiple vectors comprising expression control sequences are taught, e.g., pCMV-SPORT6 and pSPORT1).

With regard to claim 9, Strausberg teaches a cultured cell comprising the expression vector of claim 8 (p. 16899, col. 1, “cDNA library construction” heading, where cDNA libraries were prepared from tissues and cell lines comprising vectors).

With regard to claim 11, Strausberg teaches a cultured cell transfected with the vector of claim 7, or a progeny of the cell, wherein the cell expresses a polypeptide encoded by the expression vector (p. 16899, col. 1, “cDNA library construction” heading, where cDNA libraries

were prepared from tissues and cell lines comprising vectors; as evidenced by Mammalian Gene Collection (mgc.nci.nih.gov), where multiple vectors comprising expression control sequences are taught, e.g., pCMV-SPORT6 and pSPORT1).

With regard to claim 12, Strausberg teaches a cultured cell comprising the nucleic acid of claim 7 operably linked to an expression control sequence (p. 16899, col. 1, "cDNA library construction" heading, where cDNA libraries were prepared from tissues and cell lines comprising vectors; as evidenced by Mammalian Gene Collection (mgc.nci.nih.gov), where multiple vectors comprising expression control sequences are taught, e.g., pCMV-SPORT6 and pSPORT1).

With regard to claim 14, Strausberg teaches an isolated nucleic acid comprising a sequence that hybridizes under low stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO: 1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 6, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

With regard to claim 15, Strausberg teaches an isolated nucleic acid comprising a sequence that hybridizes under medium stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO:1 or the complement of SEQ ID NO: 1 (see alignment associated with claim 6, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

With regard to claim 16, Strausberg teaches an isolated nucleic acid comprising a sequence that hybridizes under high stringency conditions to a hybridization probe the sequence of which consists of SEQ ID NO: 1 or the complement of SEQ ID NO: 1 (see alignment

associated with claim 6, where this alignment comprises a sequence that would hybridize under low stringency to SEQ ID NO:1).

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

5. Claim 5 is rejected under 35 U.S.C. 103(a) as being unpatentable over Tang et al. (WO02070539; September 2002) in view of Roy et al. (Human Molecular Genetics, 2001, vol. 10, no. 20, p. 2181-2186). Tang teaches the isolation of nucleic acids and polypeptides (Abstract).

With regard to claim 5, Tang teaches an embodiment of claim 1, wherein the polypeptide, is expressed in a cell (the amino acid of SEQ ID NO:1018 of Tang has 100% identity with SEQ ID NO:2 and p. 3, lines 3-5, where the expression vector is transformed into cells; p. 4, lines 13-19, where the cells are cultured and the polypeptide is isolated).

Regarding claim 5, Tang does not explicitly teach that expression of the protein renders the cell resistant to DNA-damaging agents. Tang teaches that the protein comprises sideroflexin (p. 130, Table 2, where SEQ ID NO:1018 encodes sideroflexin). Roy teaches that sideroflexin is associated with the transport of molecules associated with oxidative DNA damage (p. 2182, col. 2, where sideroflexin transports molecules into the mitochondria, when mutated, results in

accumulations of iron in the mitochondria, which leads to oxidative DNA damage; p. 2181, where iron can promote oxidative damage).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to have extended the teachings of Tang to include the function of the protein isolated by Tang as taught by Roy as including resistance to DNA damaging agents to arrive at the claimed invention with a reasonable expectation for success. Roy teaches that mutations in sideroflexin is associated with siderocytic or sideroblastic anemias, and "an inability to efficiently produce and export heme in both of these anemias is coupled with the accumulation of iron in the mitochondria of erythrocyte precursors" (p. 2183, legend to Figure 1). Roy also teaches "iron can promote oxidative damage to vital biological structures. Iron homeostasis must, therefore, be tightly regulated" (p. 2181, col. 1). Therefore, one of ordinary skill in the art at the time the invention was made would have been motivated to have extended the teachings of Tang to include the function of the protein isolated by Tang as taught by Roy as including resistance to DNA damaging agents to arrive at the claimed invention with a reasonable expectation for success.

Conclusion

No claims are allowed.


Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stephanie K. Mummert, Ph.D. whose telephone number is 571-272-8503. The examiner can normally be reached on M-F, 9:00-5:30.

Application/Control Number:
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Art Unit: 1637

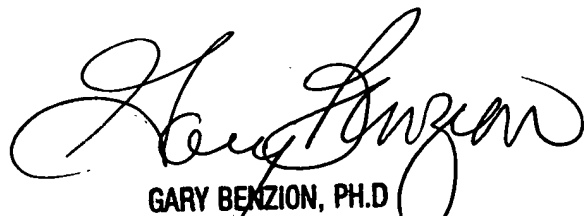
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If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.


Stephanie K Mummert, Ph.D.
Examiner
Art Unit 1637

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